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Atty Dkt. No.: 10031034-1
USSN: 10/828,907

AMENDMENT

Please incorporate the following amendments into the subject application.

In the Claims:

1. (Currently amended) A method of assessing a surface-bound polynucleotide, comprising:
 contacting a first labeled population of nucleic acids made from a non-cellular chromosome composition **synthesized by mixing pre-determined amounts of individual chromosomes** with an array of surface-bound polynucleotides; and
 evaluating binding of a surface-bound polynucleotide to said first labeled population of nucleic acids relative to binding of a second labeled population of nucleic acids made from a reference chromosome composition.
2. (Original) The method of claim 1, wherein said first and second labeled population of nucleic acids are distinguishably labeled.
3. (Original) The method of claim 2, wherein said surface-bound polynucleotide binds to the same chromosome in said non-cellular and said reference chromosome compositions.
4. (Original) The method of claim 3, wherein said chromosome is present at a predetermined ratio in said non-cellular and said reference chromosome compositions.
5. (Original) The method of claim 4, wherein said ratio is an integer selected from whole numbers and zero.
6. (Original) The method of claim 1, wherein said non-cellular chromosome composition contains at least one but less than all chromosomes from a mammalian cell.

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7. (Original) The method of claim 6, wherein said at least one chromosome is present at a relative level that does not naturally occur in said mammalian cell.

8. (Original) The method of claim 1, wherein said non-cellular chromosome composition contains all chromosomes of a mammalian cell, with one or more chromosomes present in an amount that does not naturally occur in said mammalian cell.

9. (Original) The method of claim 1, wherein said surface-bound polynucleotide is an oligonucleotide.

10. (Original) The method of claim 1, wherein said method further comprises isolating a chromosome from a mammalian cell to provide said non-cellular chromosome composition.

11. (Original) A method of assaying a candidate surface-bound polynucleotide for suitability for use in array-based comparative genome hybridization assays, comprising:

assessing binding of said candidate surface-bound polynucleotide on an array according to the method of claim 1.

12. (Original) The method of claim 11, wherein a surface-bound polynucleotide suitable for use in array-based comparative genome hybridization assays is a surface-bound polynucleotide that binds to said first and second labeled nucleic acid populations at a relative level that corresponds to the relative level of a chromosome in said chromosome compositions.

13. (Original) The method of claim 12, wherein said chromosome is a pre-determined chromosome.

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14. (Original) The method of claim 11, wherein said array comprises a plurality of different candidate surface-bound polynucleotides.

15. (Original) The method of claim 11, wherein said methods comprises assessing binding of a candidate surface-bound polynucleotide to chromosome composition probes comprising all chromosomes of an animal cell.

16. (Original) The method of claim 11, wherein the method further comprises identifying a surface-bound polynucleotide suitable for use in array-based comparative genome hybridization assays.

17. (Withdrawn) A method of producing an array, comprising,
identifying a surface-bound polynucleotide suitable for use in array-based comparative genome hybridization assays according to the method of claim 16; and
fabricating an array comprising said surface-bound polynucleotide.

18. (Withdrawn) An array of surface-bound polynucleotides, wherein at least one of said surface-bound polynucleotide has been identified using the method of claim 16.

19. (Withdrawn) A method of using an array, comprising:
interrogating an array of claim 18 with populations of labeled nucleic acids made from a first and a second chromosome compositions to provide data on the copy number of at least one nucleic acid sequence in said compositions.

20. (Withdrawn) The method of claim 19, further comprising transmitting said data from a first location to a second location.

21. (Withdrawn) The method of claim 20, wherein said second location is a remote location.

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22. (Withdrawn) The method of claim 20, further comprising receiving said data.

23. (Withdrawn) A non-cellular chromosome composition comprising at least two different chromosomes from an animal cell in relative amounts that are different to that found in said cell.

24. (Withdrawn) The composition of claim 23, wherein said non-cellular chromosome composition comprises at least one extra copy of a chromosome, relative to the chromosomes of said animal cell.

25. (Withdrawn) The composition of claim 23, wherein said non-cellular chromosome composition comprises a pre-determined number of chromosomes isolated from said mammalian cell.

26. (Withdrawn) A kit comprising:
a non-cellular chromosome composition comprising at least one chromosome isolated from an animal cell; and,
a reference chromosome composition comprising a reference chromosome;
wherein said chromosome isolated from an animal cell and said reference chromosome are the same chromosome and are present in said compositions at pre-determined relative amounts.

27. (Withdrawn) The kit of claim 26, wherein said chromosome compositions further comprise at least one other chromosome from said animal cell.

28. (Withdrawn) The kit of claim 26, further comprising instructions for performing the method of claim 1.

29. (Withdrawn) A computer-readable medium comprising:

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programming for analyzing data provided by the method of claim 11.

30. (Withdrawn) The computer-readable medium of claim 29, wherein an output of said programming is a surface-bound polynucleotide for suitability for use in array-based comparative genome hybridization assays.

31. (Withdrawn) A computer comprising the computer-readable medium of claim 29.

32. (Withdrawn) A computer implemented method, comprising:
evaluating data produced by the method of claim 11; and
identifying a surface-bound polynucleotide suitable for use in array-based comparative genome hybridization assays